SEQUENCE LISTING

<110>   Moloney, Maurice M.

        Van Rooijen, Gijs

<120>   Preparation of Heterologous Proteins on Oil Bodies

<130>   9369-292

<150>   09/893,525
<151>   2001-06-29

<150>   US 09/210,843
<151>   1998-12-15

<150>   US 08/846,021
<151>   1997-04-25

<150>   US 08/366,783
<151>   1994-12-30

<150>   US 08/142,418
<151>   1993-11-16

<150>   US 07/659,835
<151>   1991-02-22

<160>   42

<170>   PatentIn version 3.1

<210>   1
<211>   1800

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (868)..(1221)

<223>

<220>

<221> CDS

<222> (1462)..(1629)

<223>

<400> 1

```
ccatggctat acccaacctc ggtcttggtc acaccaggaa ctctctggta agctagctcc      60

actccccaga aacaaccggc gccaaattgc cggaattgct gacctgaaga cggaacatca     120

tcgtcgggtc cttgggcgat tgcggcggaa gatgggtcag cttgggcttg aggacgagac     180

ccgaatcgag tctgttgaaa ggttgttcat tgggatttgt atacggagat tggtcgtcga     240

gaggtttgag ggaaaggaca aatgggtttg gctctggaga aagagagtgc ggctttagag     300

agagaattga gaggtttaga gagagatgcg gcggcgatga cgggaggaga gacgacgagg     360

acctgcatta tcaaagcagt gacgtggtga aatttggaac ttttaagagg cagatagatt     420

tattatttgt atccattttc ttcattgttc tagaatgtcg cggaacaaat tttaaaacta     480

aatcctaaat ttttctaatt ttgttgccaa tagtggatat gtgggccgta tagaaggaat     540

ctattgaagg cccaaaccca tactgacgag cccaaaggtt cgtttgcgt tttatgtttc      600

ggttcgatgc caacgccaca ttctgagcta ggcaaaaaac aaacgtgtct ttgaatagac     660

tcctctcgtt aacacatgca gcggctgcat ggtgacgcca ttaacacgtg cctacaatt      720

gcatgatgtc tccattgaca cgtgacttct cgtctccttt cttaatatat ctaacaaaca     780

ctcctacctc ttccaaaata tatacacatc tttttgatca atctctcatt caaaatctca     840

ttctctctag taaacaagaa caaaaaa atg gcg gat aca gct aga gga acc cat     894
                                Met Ala Asp Thr Ala Arg Gly Thr His
                                 1               5

cac gat atc atc ggc aga gac cag tac ccg atg atg ggc cga gac cga     942
His Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg
10              15                  20                  25

gac cag tac cag atg tcc gga cga gga tct gac tac tcc aag tct agg     990
Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg
                30                  35                  40
```

```
cag att gct aaa gct gca act gct gtc aca gct ggt ggt tcc ctc ctt    1038
Gln Ile Ala Lys Ala Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu
            45              50              55

gtt ctc tcc agc ctt acc ctt gtt gga act gtc ata gct ttg act gtt    1086
Val Leu Ser Ser Leu Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val
            60              65              70

gca aca cct ctg ctc gtt atc ttc agc cca atc ctt gtc ccg gct ctc    1134
Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu
            75              80              85

atc aca gtt gca ctc ctc atc acc ggt ttt ctt tcc tct gga ggg ttt    1182
Ile Thr Val Ala Leu Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe
90              95              100             105

ggc att gcc gct ata acc gtt ttc tct tgg att tac aag taagcacaca    1231
Gly Ile Ala Ala Ile Thr Val Phe Ser Trp Ile Tyr Lys
            110             115

tttatcatct tacttcataa ttttgtgcaa tatgtgcatg catgtgttga gccagtagct    1291

ttggatcaat tttttggtc gaataacaaa tgtaacaata agaaattgca aattctaggg    1351

aacatttggt taactaaata cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat    1411

catctatata ggtaaaatgc ttggtatgat acctattgat tgtgaatagg tac gca      1467
                                                        Tyr Ala
                                                        120

acg gga gag cac cca cag gga tca gac aag ttg gac agt gca agg atg    1515
Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala Arg Met
                125             130             135

aag ttg gga agc aaa gct cag gat ctg aaa gac aga gct cag tac tac    1563
Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr
            140             145             150

gga cag caa cat act ggt ggg gaa cat gac cgt gac cgt act cgt ggt    1611
Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr Arg Gly
        155             160             165

ggc cag cac act act taa gttaccccac tgatgtcatc gtcatagtcc          1659
Gly Gln His Thr Thr
    170

aataactcca atgtcgggga gttagtttat gaggaataaa gtgtttagaa tttgatcagg    1719

gggagataat aaaagccgag tttgaatctt tttgttataa gtaatgttta tgtgtgtttc    1779

tatatgttgt caaatggtac c                                          1800
```

<210> 2

<211> 118

<212> PRT

<213> Arabidopsis thaliana

<400> 2

```
Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
1               5               10              15


Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
            20              25              30


Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
        35              40              45


Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
    50              55              60


Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65              70              75              80


Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
            85              90              95


Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
            100             105             110


Phe Ser Trp Ile Tyr Lys
        115
```

<210> 3

<211> 55

<212> PRT

<213> Arabidopsis thaliana

<400> 3

```
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1               5               10              15


Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
            20              25              30


Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
        35              40              45


Arg Gly Gly Gln His Thr Thr
    50              55
```

<210> 4

<211> 564

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(561)

<223>

<400> 4

```
atg gcg gat aca gct aga acc cat cac gat gtc aca agt cga gat cag        48
Met Ala Asp Thr Ala Arg Thr His His Asp Val Thr Ser Arg Asp Gln
1               5                   10                  15

tat ccc cga gac cga gac cag tat tct atg atc ggt cga gac cgt gac        96
Tyr Pro Arg Asp Arg Asp Gln Tyr Ser Met Ile Gly Arg Asp Arg Asp
                20                  25                  30

cag tac tct atg atg ggc cga gac cga gac cag tac aac atg tat ggt       144
Gln Tyr Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn Met Tyr Gly
            35                  40                  45

cga gac tac tcc aag tct aga cag att gct aag gct gtt acc gca gtc       192
Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val Thr Ala Val
        50                  55                  60

acg gcg ggt ggg tcc ctc ctt gtc ctc tcc agt ctc acc ctt gtt ggt       240
Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly
65                  70                  75                  80

act gtc att gct ttg act gtt gcc act cca ctc ctc gtt atc ttt agc       288
Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser
                85                  90                  95

cca atc ctc gtg ccg gct ctc atc acc gta gca ctt ctc atc act ggc       336
Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly
            100                 105                 110

ttt ctc tcc tct ggt ggg ttt gcc att gca gct ata acc gtc ttc tcc       384
Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr Val Phe Ser
            115                 120                 125

tgg atc tat aag tac gca acg gga gag cac cca cag ggg tca gat aag       432
Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys
        130                 135                 140

ttg gac agt gca agg atg aag ctg gga acc aaa gct cag gat att aaa       480
Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln Asp Ile Lys
145                 150                 155                 160

gac aga gct caa tac tac gga cag caa cat aca ggt ggt gag cat gac       528
Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp
                165                 170                 175

cgt gac cgt act cgt ggt ggc cag cac act act taa                       564
Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
                180                 185
```


<210> 5

<211> 187

<212> PRT

<213> Brassica napus

<400> 5

Met Ala Asp Thr Ala Arg Thr His His Asp Val Thr Ser Arg Asp Gln
1   5   10   15

Tyr Pro Arg Asp Arg Asp Gln Tyr Ser Met Ile Gly Arg Asp Arg Asp
            20   25   30

Gln Tyr Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn Met Tyr Gly
        35   40   45

Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val Thr Ala Val
    50   55   60

Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly
65   70   75   80

Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser
                85   90   95

Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly
            100   105   110

Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr Val Phe Ser
        115   120   125

Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys
    130   135   140

Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln Asp Ile Lys
145   150   155   160

Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp
                165   170   175

Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
            180   185

<210> 6

<211> 2733

<212> DNA

<213> Artificial Sequence

```
<220>

<223>   Oleosin-Chymosin Fusion

<220>

<221>   CDS

<222>   (850)..(1203)

<223>


<220>

<221>   CDS

<222>   (1444)..(2727)

<223>


<400>   6
ataagcttgc atgcctgcgg aactctctgg taagctagct ccactcccca gaaacaaccg      60

gcgccaaatt gccggaattg ctgacctgaa gacggaacat catcgtcggg tccttgggcg     120

attgcggcgg aagatgggtc agcttgggct tgaggacgag acccgaatcg agtctgttga     180

aaggttgttc attgggattt gtatacggag attggtcgtc gagaggtttg agggaaagga     240

caaatgggtt tggctctgga gaaagagagt gcggctttag agagagaatt gagaggttta     300

gagagagatg cggcggcgat gacgggagga gagacgacga ggacctgcat tatcaaagca     360

gtgacgtggt gaaatttgga acttttaaga ggcagataga tttattattt gtatccattt     420

tcttcattgt tctagaatgt cgcggaacaa attttaaaac taaatcctaa attttctaa      480

ttttgttgcc aatagtggat atgtgggccg tatagaagga atctattgaa ggcccaaacc     540

catactgacg agcccaaagg ttcgttttgc gttttatgtt tcggttcgat gccaacgcca     600

cattctgagc taggcaaaaa acaaacgtgt ctttgaatag actcctctcg ttaacacatg     660

cagcggctgc atggtgacgc cattaacacg tggcctacaa ttgcatgatg tctccattga     720

cacgtgactt ctcgtctcct ttcttaatat atctaacaaa cactcctacc tcttccaaaa     780

tatatacaca tctttttgat caatctctca ttcaaaatct cattctctct agtaaacaag     840

aacaaaaaa atg gcg gat aca gct aga gga acc cat cac gat atc atc ggc     891
           Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly
            1               5                  10

aga gac cag tac ccg atg atg ggc cga gac cga gac cag tac cag atg      939
Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met
15              20               25              30

tcc gga cga gga tct gac tac tcc aag tct agg cag att gct aaa gct      987
Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala
             35              40              45
```

```
gca act gct gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt      1035
Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu
            50                  55                  60

acc ctt gtt gga act gtc ata gct ttg act gtt gca aca cct ctg ctc      1083
Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu
            65                  70                  75

gtt atc ttc agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc      1131
Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu
        80                  85                  90

ctc atc acc ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata      1179
Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile
95                  100                 105                 110

acc gtt ttc tct tgg att tac aag taagcacaca tttatcatct tacttcataa    1233
Thr Val Phe Ser Trp Ile Tyr Lys
                115

ttttgtgcaa tatgtgcatg catgtgttga gccagtagct ttggatcaat tttttggtc    1293

gaataacaaa tgtaacaata agaaattgca aattctaggg aacatttggt taactaaata   1353

cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc   1413

ttggtatgat acctattgat tgtgaatagg tac gca acg gga gag cac cca cag    1467
                                  Tyr Ala Thr Gly Glu His Pro Gln
                                      120                 125

gga tca gac aag ttg gac agt gca agg atg aag ttg gga agc aaa gct      1515
Gly Ser Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala
            130                 135                 140

cag gat ctg aaa gac aga gct cag tac tac gga cag caa cat act ggt      1563
Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly
            145                 150                 155

ggg gaa cat gac cgt gac cgt act cgt ggt ggc cag cac act act ctc      1611
Gly Glu His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Leu
        160                 165                 170

gtt cca cga gga tcc atg gct gag atc acc agg atc cct ctg tac aaa      1659
Val Pro Arg Gly Ser Met Ala Glu Ile Thr Arg Ile Pro Leu Tyr Lys
175                 180                 185                 190

ggc aag tct ctg agg aag gcg ctg aag gag cat ggg ctt ctg gag gac      1707
Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu Leu Glu Asp
            195                 200                 205

ttc ctg cag aaa cag cag tat ggc atc agc agc aag tac tcc ggc ttc      1755
Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr Ser Gly Phe
            210                 215                 220

ggg gag gtg gcc agc gtg ccc ctg acc aac tac ctg gat agt cag tac      1803
Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser Gln Tyr
            225                 230                 235

ttt ggg aag atc tac ctc ggg acc ccg ccc cag gag ttc acc gtg ctg      1851
Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr Val Leu
            240                 245                 250

ttt gac act ggc tcc tct gac ttc tgg gta ccc tct atc tac tgc aag      1899
Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr Cys Lys
255                 260                 265                 270
```

```
agc aat gcc tgc aaa aac cac cag cgc ttc gac ccg aga aag tcg tcc      1947
Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys Ser Ser
                275                 280                 285

acc ttc cag aac ctg ggc aag ccc ctg tct atc cac tac ggg aca ggc      1995
Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly Thr Gly
                290                 295                 300

agc atg cag ggc atc ctg ggc tat gac acc gtc act gtc tcc aac att      2043
Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser Asn Ile
                305                 310                 315

gtg gac atc cag cag aca gta ggc ctg agc acc cag gag ccc ggg gac      2091
Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro Gly Asp
                320                 325                 330

gtc ttc acc tat gcc gaa ttc gac ggg atc ctg ggg atg gcc tac ccc      2139
Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro
335                 340                 345                 350

tcg ctc gcc tca gag tac tcg ata ccc gtg ttt gac aac atg atg aac      2187
Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met Met Asn
                355                 360                 365

agg cac ctg gtg gcc caa gac ctg ttc tcg gtt tac atg gac agg aat      2235
Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp Arg Asn
                370                 375                 380

ggc cag gag agc atg ctc acg ctg ggg gcc atc gac ccg tcc tac tac      2283
Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser Tyr Tyr
                385                 390                 395

aca ggg tcc ctg cac tgg gtg ccc gtg aca gtg cag cag tac tgg cag      2331
Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr Trp Gln
                400                 405                 410

ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gtg gcc tgt gag      2379
Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala Cys Glu
415                 420                 425                 430

ggt ggc tgt cag gcc atc ttg gac acg ggc acc tcc aag ctg gtc ggg      2427
Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu Val Gly
                435                 440                 445

ccc agc agc gac atc ctc aac atc cag cag gcc att gga gcc aca cag      2475
Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala Thr Gln
                450                 455                 460

aac cag tac ggt gag ttt gac atc gac tgc gac aac ctg agc tac atg      2523
Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu Ser Tyr Met
                465                 470                 475

ccc act gtg gtc ttt gag atc aat ggc aaa atg tac cca ctg acc ccc      2571
Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro Leu Thr Pro
480                 485                 490

tcc gcc tat acc agc caa gac cag ggc ttc tgt acc agt ggc ttc cag      2619
Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser Gly Phe Gln
495                 500                 505                 510

agt gaa aat cat tcc cag aaa tgg atc ctg ggg gat gtt ttc atc cga      2667
Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val Phe Ile Arg
                515                 520                 525

gag tat tac agc gtc ttt gac agg gcc aac aac ctc gtg ggg ctg gcc      2715
```

```
Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val Gly Leu Ala
            530                 535             540

aaa gcc atc tga aagctt                                              2733
Lys Ala Ile
        545
```

<210> 7

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Oleosin-Chymosin Fusion

<400> 7

```
Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
1               5               10              15


Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
            20              25              30


Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
        35              40              45


Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
    50              55              60


Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65              70              75              80


Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
            85              90              95


Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
            100             105             110


Phe Ser Trp Ile Tyr Lys
        115
```

<210> 8

<211> 427

<212> PRT

<213> Artificial Sequence

<220>

<223> Oleosin-Chymosin Fusion

<400> 8

Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1   5   10   15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
            20   25   30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
        35   40   45

Arg Gly Gly Gln His Thr Thr Leu Val Pro Arg Gly Ser Met Ala Glu
    50   55   60

Ile Thr Arg Ile Pro Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu
65   70   75   80

Lys Glu His Gly Leu Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly
            85   90   95

Ile Ser Ser Lys Tyr Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu
            100   105   110

Thr Asn Tyr Leu Asp Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr
        115   120   125

Pro Pro Gln Glu Phe Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe
    130   135   140

Trp Val Pro Ser Ile Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln
145   150   155   160

Arg Phe Asp Pro Arg Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro
            165   170   175

Leu Ser Ile His Tyr Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr
            180   185   190

Asp Thr Val Thr Val Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly
        195   200   205

Leu Ser Thr Gln Glu Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp
    210   215   220

Gly Ile Leu Gly Met Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile
225   230   235   240

```
Pro Val Phe Asp Asn Met Met Asn Arg His Leu Val Ala Gln Asp Leu
            245                 250                 255

Phe Ser Val Tyr Met Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu
            260                 265                 270

Gly Ala Ile Asp Pro Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro
            275                 280                 285

Val Thr Val Gln Gln Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile
            290                 295                 300

Ser Gly Val Val Val Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp
305                 310                 315                 320

Thr Gly Thr Ser Lys Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile
            325                 330                 335

Gln Gln Ala Ile Gly Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile
            340                 345                 350

Asp Cys Asp Asn Leu Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn
            355                 360                 365

Gly Lys Met Tyr Pro Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln
            370                 375                 380

Gly Phe Cys Thr Ser Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp
385                 390                 395                 400

Ile Leu Gly Asp Val Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg
            405                 410                 415

Ala Asn Asn Leu Val Gly Leu Ala Lys Ala Ile
            420                 425
```

```
<210>   9

<211>   5

<212>   PRT

<213>   Artificial Sequence


<220>

<223>   Thrombin Cleavage Site

<400>   9

Leu Val Pro Arg Gly
```

```
1                    5


<210>  10

<211>  4

<212>  PRT

<213>  Artificial Sequence


<220>

<223>  Factor Xa Cleavage Site

<400>  10

Phe Glu Gly Arg
1


<210>  11

<211>  4

<212>  PRT

<213>  Artificial Sequence


<220>

<223>  Collagenase Cleavage Site

<400>  11

Pro Leu Gly Pro
1


<210>  12

<211>  7

<212>  PRT

<213>  Artificial Sequence


<220>

<223>  TEV Protease

<400>  12

Glu Asn Leu Tyr Phe Gln Gly
1                    5


<210>  13

<211>  14
```

```
<212>  DNA

<213>  Artificial Sequence


<220>

<223>  Carrot

<400>  13
tctcaacaat ggca                                                    14


<210>  14

<211>  14

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  Maize

<400>  14
cggcagcaat ggcg                                                    14


<210>  15

<211>  22

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  GVR1O 5' Primer

<400>  15
cactgcagga actctctggt aa                                           22


<210>  16

<211>  31

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  ALP1 Primer

<400>  16
```

```
ctacccggga tcctgtttac tagagagaat g                                    31
```

```
<210>  17

<211>  62

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  GVR01 Primer

<400>  17
aatcccatgg atcctcgtgg aacgagagta gtgtgctggc caccacgagt acggtcacgg    60

tc                                                                    62


<210>  18

<211>  24

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  GVR10 3' Primer

<400>  18
cactgcagga actctctggt aagc                                            24


<210>  19

<211>  29

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  GVR20 Primer

<400>  19
gaggatccat ggtacgtcct gtagaaacc                                       29


<210>  20

<211>  17

<212>  DNA

<213>  Artificial Sequence
```

<220>

<223> Primer GVR20

<400> 20
gtaaaacgac ggccagt   17

<210> 21

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide

<400> 21

Leu Val Pro Arg Gly Ser
1   5

<210> 22

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> IL-1-B Peptide

<400> 22

Val Gln Gly Glu Glu Ser Asn Asp Lys
1   5

<210> 23

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> OleoPromK Primer

<400> 23

cgcggtacca tggctatacc caacctcg   28

<210>   24

<211>   28

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   3' Primer

<400>   24
cgcatcgatg ttcttgttta ctagagag   28

<210>   25

<211>   36

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   5'-GUS-Cla Primer

<400>   25
gccatcgatc atatgttacg tcctgtagaa acccca   36

<210>   26

<211>   37

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   3'-GUS-FX-Bam Primer

<400>   26
cgcggatcct cttccttcga tttgtttgcc tccctgc   37

<210>   27

<211>   27

<212>   DNA

<213>   Artificial Sequence

<220>

<223> 5'-Bam-Oleo

<400> 27
cgcggatcca tggcggatac agctaga   27

<210> 28

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-Oleo-Xba

<400> 28
tgctctagac gatgacatca gtggggtaac ttaagt   36

<210> 29

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Spacer

<400> 29

Leu Val Pro Arg Gly Ser
1   5

<210> 30

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 30
atctctagaa ttcaactact cttgctcaaa g   31

<210> 31

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 31
gggttgctcg agatttctaa tcaatttat   29

<210> 32

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> GVR979 Primer

<400> 32
taccatgggg tcaaagacgg ag   22

<210> 33

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> GVR980 Primer

<400> 33
atccatggcg tagtatgctg tcttgtct   28

<210> 34

<211> 748

<212> DNA

<213> Arabidopsis caleosin

<400> 34
taccatgggg tcaaagacgg agatgatgga gagagacgca atggctacgg tggctcccta   60

```
tgcgccggtc acttaccatc gccgtgctcg tgttgacttg gatgatagac ttcctaaacc   120

ttatatgcca agagcattgc aagcaccaga cagagaacac ccgtacggaa ctccaggcca   180

taagaattac ggacttagtg ttcttcaaca gcatgtctcc ttcttcgata tcgatgataa   240

tggcatcatt taccccttggg agacctactc tggactgcga atgcttggtt tcaatatcat   300

tgggtcgctt ataatagccg ctgttatcaa cctgacccttt agctatgcca ctcttccggg   360

gtggttacct tcacctttct tccctatata catacacaac atacacaagt caaagcatgg   420

aagtgattca aaaacatatg acaatgaagg aaggtttatg ccggtgaatc ttgagttgat   480

atttagcaaa tatgcgaaaa ccttgccaga caagttgagt cttggagaac tatgggagat   540

gacagaagga aaccgtgacg cttgggacat ttttggatgg atcgcaggca aaatagagtg   600

gggactgttg tacttgctag caagggatga agaagggttt ttgtcaaaag aagctattag   660

gcggtgtttc gatggaagct tgttcgagta ctgtgccaaa atctacgctg gtatcagtga   720

agacaagaca gcatactacg ccatggat                                     748
```

```
<210>  35
<211>  738
<212>  DNA
<213>  Arabidopsis caleosin


<400>  35
atggggtcaa agacggagat gatggagaga gacgcaatgg ctacggtggc tccctatgcg    60

ccggtcactt accaccgccg tgctcgtgtt gacttggatg atagacttcc taaaccttat   120

atgccaagag cattgcaagc accagacaga gaacaccgt acggaactcc aggccataag   180

aattacggac ttagtgttct tcaacagcat gtctccttct tcgatatcga tgataatggc   240

atcatttacc cttgggagac ctactctgga ctgcgaatgc ttggtttcaa tatcattggg   300

tcgcttataa tagccgctgt tatcaacctg acccttagct atgccactct tccggggtgg   360

ttaccttcac ctttcttccc tatatacata cacaacatac acaagtcaaa gcatggaagt   420

gattcaaaaa catatgacaa tgaaggaagg tttatgccgg tgaatcttga gttgatattt   480

agcaaatatg cgaaaacctt gccagacaag ttgagtcttg gagaactatg ggagatgaca   540

gaaggaaacc gtgacgcttg gacatttttt ggatggatcg caggcaaaat agagtgggga   600

ctgttgtact tgctagcaag ggatgaagaa gggttttttgt caaaagaagc tattaggcgg   660

tgtttcgatg gaagcttgtt cgagtactgt gccaaaatct acgctggtat cagtgaagac   720

aagacagcat actactaa                                                738
```

```
<210>  36
<211>  4652
```

<212> DNA

<213> Artificial Sequence

<220>

<223> Phas-GUS-phas

<220>

<221> CDS

<222> (1548)..(3359)

<223>

<400> 36
gaattcattg tactcccagt atcattatag tgaaagtttt ggctctctcg ccggtggttt   60

tttacctcta tttaaagggg ttttccacct aaaaattctg gtatcattct cactttactt   120

gttactttaa tttctcataa tctttggttg aaattatcac gcttccgcac acgatatccc   180

tacaaattta ttatttgtta aacattttca aaccgcataa aattttatga agtcccgtct   240

atctttaatg tagtctaaca ttttcatatt gaaatatata atttacttaa ttttagcgtt   300

ggtagaaagc ataaagattt attcttattc ttcttcatat aaatgtttaa tatacaatat   360

aaacaaattc tttaccttaa gaaggatttc ccattttata ttttaaaaat atatttatca   420

aatattttc aaccacgtaa atctcataat aataagttgt ttcaaaagta ataaaattta   480

actccataat ttttttattc gactgatctt aaagcaacac ccagtgacac aactagccat   540

ttttttcttt gaataaaaaa atccaattat cattgtattt tttttataca atgaaaattt   600

caccaaacaa tcatttgtgg tatttctgaa gcaagtcatg ttatgcaaaa ttctataatt   660

cccatttgac actacggaag taactgaaga tctgctttta catgcgagac acatcttcta   720

aagtaatttt aataatagtt actatattca agatttcata tatcaaatac tcaatattac   780

ttctaaaaaa ttaattagat ataattaaaa tattactttt ttaattttaa gtttaattgt   840

tgaatttgtg actattgatt tattattcta ctatgtttaa attgttttat agatagttta   900

aagtaaatat aagtaatgta gtagagtgtt agagtgttac cctaaaccat aaactataac   960

atttatggtg gactaatttt catatatttc ttattgcttt tacctttct tggtatgtaa   1020

gtccgtaact agaattacag tgggttgcca tgacactctg tggtcttttg gttcatgcat   1080

gggtcttgcg caagaaaag acaagaaca aagaaaaaag acaaaacaga gagacaaaac   1140

gcaatcacac aaccaactca aattagtcac tggctgatca agatcgccgc gtccatgtat   1200

gtctaaatgc catgcaaagc aacacgtgct taacatgcac tttaaatggc tcacccatct   1260

caacccacac acaaacacat tgcctttttc ttcatcatca ccacaaccac ctgtatatat   1320

```
tcattctctt ccgccacctc aatttcttca cttcaacaca cgtcaacctg catatgcgtg    1380

tcatcccatg cccaaatctc catgcatgtt ccaaccacct tctctcttat ataataccta    1440

taaatacctc taatatcact cacttctttc atcatccatc catccagagt actactactc    1500

tactactata ataccccaac ccaactcata ttcaatacta ctctacc atg gtc tta      1556
                                                    Met Val Leu
                                                     1
```

```
cgt cct gta gaa acc cca acc cgt gaa atc aaa aaa ctc gac ggc ctg      1604
Arg Pro Val Glu Thr Pro Thr Arg Glu Ile Lys Lys Leu Asp Gly Leu
     5                  10                  15
```

```
tgg gca ttc agt ctg gat cgc gaa aac tgt gga att gat cag cgt tgg      1652
Trp Ala Phe Ser Leu Asp Arg Glu Asn Cys Gly Ile Asp Gln Arg Trp
20                  25                  30                  35
```

```
tgg gaa agc gcg tta caa gaa agc cgg gca att gct gtg cca ggc agt      1700
Trp Glu Ser Ala Leu Gln Glu Ser Arg Ala Ile Ala Val Pro Gly Ser
                 40                  45                  50
```

```
ttt aac gat cag ttc gcc gat gca gat att cgt aat tat gcg ggc aac      1748
Phe Asn Asp Gln Phe Ala Asp Ala Asp Ile Arg Asn Tyr Ala Gly Asn
                 55                  60                  65
```

```
gtc tgg tat cag cgc gaa gtc ttt ata ccg aaa ggt tgg gca ggc cag      1796
Val Trp Tyr Gln Arg Glu Val Phe Ile Pro Lys Gly Trp Ala Gly Gln
                 70                  75                  80
```

```
cgt atc gtg ctg cgt ttc gat gcg gtc act cat tac ggc aaa gtg tgg      1844
Arg Ile Val Leu Arg Phe Asp Ala Val Thr His Tyr Gly Lys Val Trp
     85                  90                  95
```

```
gtc aat aat cag gaa gtg atg gag cat cag ggc ggc tat acg cca ttt      1892
Val Asn Asn Gln Glu Val Met Glu His Gln Gly Gly Tyr Thr Pro Phe
100                 105                 110                 115
```

```
gaa gcc gat gtc acg ccg tat gtt att gcc ggg aaa agt gta cgt atc      1940
Glu Ala Asp Val Thr Pro Tyr Val Ile Ala Gly Lys Ser Val Arg Ile
                 120                 125                 130
```

```
acc gtt tgt gtg aac aac gaa ctg aac tgg cag act atc ccg ccg gga      1988
Thr Val Cys Val Asn Asn Glu Leu Asn Trp Gln Thr Ile Pro Pro Gly
                 135                 140                 145
```

```
atg gtg att acc gac gaa aac ggc aag aaa aag cag tct tac ttc cat      2036
Met Val Ile Thr Asp Glu Asn Gly Lys Lys Lys Gln Ser Tyr Phe His
                 150                 155                 160
```

```
gat ttc ttt aac tat gcc gga atc cat cgc agc gta atg ctc tac acc      2084
Asp Phe Phe Asn Tyr Ala Gly Ile His Arg Ser Val Met Leu Tyr Thr
                 165                 170                 175
```

```
acg ccg aac acc tgg gtg gac gat atc acc gtg gtg acg cat gtc gcg      2132
Thr Pro Asn Thr Trp Val Asp Asp Ile Thr Val Val Thr His Val Ala
180                 185                 190                 195
```

```
caa gac tgt aac cac gcg tct gtt gac tgg cag gtg gtg gcc aat ggt      2180
Gln Asp Cys Asn His Ala Ser Val Asp Trp Gln Val Val Ala Asn Gly
                 200                 205                 210
```

```
gat gtc agc gtt gaa ctg cgt gat gcg gat caa cag gtg gtt gca act      2228
Asp Val Ser Val Glu Leu Arg Asp Ala Asp Gln Gln Val Val Ala Thr
                 215                 220                 225
```

```
gga caa ggc act agc ggg act ttg caa gtg gtg aat ccg cac ctc tgg     2276
Gly Gln Gly Thr Ser Gly Thr Leu Gln Val Val Asn Pro His Leu Trp
        230                 235                 240

caa ccg ggt gaa ggt tat ctc tat gaa ctg tgc gtc aca gcc aaa agc     2324
Gln Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Cys Val Thr Ala Lys Ser
        245                 250                 255

cag aca gag tgt gat atc tac ccg ctt cgc gtc ggc atc cgg tca gtg     2372
Gln Thr Glu Cys Asp Ile Tyr Pro Leu Arg Val Gly Ile Arg Ser Val
260                 265                 270                 275

gca gtg aag ggc caa cag ttc ctg att aac cac aaa ccg ttc tac ttt     2420
Ala Val Lys Gly Gln Gln Phe Leu Ile Asn His Lys Pro Phe Tyr Phe
                280                 285                 290

act ggc ttt ggt cgt cat gaa gat gcg gac tta cgt ggc aaa gga ttc     2468
Thr Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg Gly Lys Gly Phe
            295                 300                 305

gat aac gtg ctg atg gtg cac gac cac gca tta atg gac tgg att ggg     2516
Asp Asn Val Leu Met Val His Asp His Ala Leu Met Asp Trp Ile Gly
        310                 315                 320

gcc aac tcc tac cgt acc tcg cat tac cct tac gct gaa gag atg ctc     2564
Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu Met Leu
        325                 330                 335

gac tgg gca gat gaa cat ggc.atc gtg gtg att gat gaa act gct gct     2612
Asp Trp Ala Asp Glu His Gly Ile Val Val Ile Asp Glu Thr Ala Ala
340                 345                 350                 355

gtc ggc ttt tcg ctc tct tta ggc att ggt ttc gaa gcg ggc aac aag     2660
Val Gly Phe Ser Leu Ser Leu Gly Ile Gly Phe Glu Ala Gly Asn Lys
            360                 365                 370

ccg aaa gaa ctg tac agc gaa gag gca gtc aac ggg gaa act cag caa     2708
Pro Lys Glu Leu Tyr Ser Glu Glu Ala Val Asn Gly Glu Thr Gln Gln
            375                 380                 385

gcg cac tta cag gcg att aaa gag ctg ata gcg cgt gac aaa aac cac     2756
Ala His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp Lys Asn His
        390                 395                 400

cca agc gtg gtg atg tgg agt att gcc aac gaa ccg gat acc cgt ccg     2804
Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp Thr Arg Pro
        405                 410                 415

caa ggt gca cgg gaa tat ttc gcg cca ctg gcg gaa gca acg cgt aaa     2852
Gln Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Glu Ala Thr Arg Lys
420                 425                 430                 435

ctc gac ccg acg cgt ccg atc acc tgc gtc aat gta atg ttc tgc gac     2900
Leu Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val Met Phe Cys Asp
                440                 445                 450

gct cac acc gat acc atc agc gat ctc ttt gat gtg ctg tgc ctg aac     2948
Ala His Thr Asp Thr Ile Ser Asp Leu Phe Asp Val Leu Cys Leu Asn
            455                 460                 465

cgt tat tac gga tgg tat gtc caa agc ggc gat ttg gaa acg gca gag     2996
Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu Thr Ala Glu
        470                 475                 480

aag gta ctg gaa aaa gaa ctt ctg gcc tgg cag gag aaa ctg cat cag     3044
Lys Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys Leu His Gln
```

```
      485                    490                    495

ccg att atc atc acc gaa tac ggc gtg gat acg tta gcc ggg ctg cac    3092
Pro Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala Gly Leu His
500                    505                    510                    515

tca atg tac acc gac atg tgg agt gaa gag tat cag tgt gca tgg ctg    3140
Ser Met Tyr Thr Asp Met Trp Ser Glu Glu Tyr Gln Cys Ala Trp Leu
                   520                    525                    530

gat atg tat cac cgc gtc ttt gat cgc gtc agc gcc gtc gtc ggt gaa    3188
Asp Met Tyr His Arg Val Phe Asp Arg Val Ser Ala Val Val Gly Glu
               535                    540                    545

cag gta tgg aat ttc gcc gat ttt gcg acc tcg caa ggc ata ttg cgc    3236
Gln Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Ile Leu Arg
           550                    555                    560

gtt ggc ggt aac aag aaa ggg atc ttc act cgc gac cgc aaa ccg aag    3284
Val Gly Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp Arg Lys Pro Lys
       565                    570                    575

tcg gcg gct ttt ctg ctg caa aaa cgc tgg act ggc atg aac ttc ggt    3332
Ser Ala Ala Phe Leu Leu Gln Lys Arg Trp Thr Gly Met Asn Phe Gly
580                    585                    590                    595

gaa aaa ccg cag cag gga ggc aaa caa tgaatcaaca actctcctgg          3379
Glu Lys Pro Gln Gln Gly Gly Lys Gln
                   600

cgcaccatcg tcggctacag cctcggtgga attcgatatc aagcttaaat aagtatgaac  3439

taaaatgcat gtaggtgtaa gagctcatgg agagcatgga atattgtatc cgaccatgta  3499

acagtataat aactgagctc catctcactt cttctatgaa taaacaaagg atgttatgat  3559

atattaacac tctatctatg caccttattg ttctatgata aatttcctct tattattata  3619

aatcatctga atcgtgacgg cttatggaat gcttcaaata gtacaaaaac aaatgtgtac  3679

tataagactt tctaaacaat tctaacttta gcattgtgaa cgagacataa gtgttaagaa  3739

gacataacaa ttataatgga agaagtttgt ctccatttat atattatata ttacccactt  3799

atgtattata ttaggatgtt aaggagacat aacaattata aagagagaag tttgtatcca  3859

tttatatatt atatactacc catttatata ttatacttat ccacttattt aatgtcttta  3919

taaggtttga tccatgatat ttctaatatt ttagttgata tgtatatgaa agggtactat  3979

ttgaactctc ttactctgta taaaggttgg atcatcctta aagtgggtct atttaatttt  4039

attgcttctt acagataaaa aaaaaattat gagttggttt gataaaatat tgaaggattt  4099

aaaataataa taaataataa ataacatata atatatgtat ataaatttat tataatataa  4159

catttatcta taaaaaagta aatattgtca taaatctata caatcgttta gccttgctgg  4219

acgactctca attatttaaa cgagagtaaa catatttgac ttttttggtta tttaacaaat  4279

tattatttaa cactatatga aatttttttt ttttatcggc aaggaaataa aattaaatta  4339

ggagggacaa tggtgtgtcc caatccttat acaaccaact tccacaggaa ggtcaggtcg  4399

gggacaacaa aaaaacaggc aagggaaatt ttttaatttg ggttgtcttg tttgctgcat  4459
```

aatttatgca gtaaaacact acacataacc cttttagcag tagagcaatg gttgaccgtg   4519

tgcttagctt cttttatttt attttttat cagcaaagaa taaataaaat aaaatgagac   4579

acttcaggga tgtttcaacc cttatacaaa accccaaaaa caagtttcct agcaccctac   4639

caactaaggt acc   4652

<210>   37

<211>   604

<212>   PRT

<213>   Artificial Sequence

<220>

<223>   Phas-GUS-phas

<400>   37

```
Met Val Leu Arg Pro Val Glu Thr Pro Thr Arg Glu Ile Lys Lys Leu
1               5                   10                  15


Asp Gly Leu Trp Ala Phe Ser Leu Asp Arg Glu Asn Cys Gly Ile Asp
            20                  25                  30


Gln Arg Trp Trp Glu Ser Ala Leu Gln Glu Ser Arg Ala Ile Ala Val
        35                  40                  45


Pro Gly Ser Phe Asn Asp Gln Phe Ala Asp Ala Asp Ile Arg Asn Tyr
    50                  55                  60


Ala Gly Asn Val Trp Tyr Gln Arg Glu Val Phe Ile Pro Lys Gly Trp
65                  70                  75                  80


Ala Gly Gln Arg Ile Val Leu Arg Phe Asp Ala Val Thr His Tyr Gly
            85                  90                  95


Lys Val Trp Val Asn Asn Gln Glu Val Met Glu His Gln Gly Gly Tyr
            100                 105                 110


Thr Pro Phe Glu Ala Asp Val Thr Pro Tyr Val Ile Ala Gly Lys Ser
        115                 120                 125


Val Arg Ile Thr Val Cys Val Asn Asn Glu Leu Asn Trp Gln Thr Ile
    130                 135                 140


Pro Pro Gly Met Val Ile Thr Asp Glu Asn Gly Lys Lys Lys Gln Ser
145                 150                 155                 160


Tyr Phe His Asp Phe Phe Asn Tyr Ala Gly Ile His Arg Ser Val Met
```

```
                165                   170                   175

Leu Tyr Thr Thr Pro Asn Thr Trp Val Asp Asp Ile Thr Val Val Thr
        180             185             190

His Val Ala Gln Asp Cys Asn His Ala Ser Val Asp Trp Gln Val Val
        195             200             205

Ala Asn Gly Asp Val Ser Val Glu Leu Arg Asp Ala Asp Gln Gln Val
    210             215             220

Val Ala Thr Gly Gln Gly Thr Ser Gly Thr Leu Gln Val Val Asn Pro
225             230             235             240

His Leu Trp Gln Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Cys Val Thr
            245             250             255

Ala Lys Ser Gln Thr Glu Cys Asp Ile Tyr Pro Leu Arg Val Gly Ile
        260             265             270

Arg Ser Val Ala Val Lys Gly Gln Gln Phe Leu Ile Asn His Lys Pro
        275             280             285

Phe Tyr Phe Thr Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg Gly
    290             295             300

Lys Gly Phe Asp Asn Val Leu Met Val His Asp His Ala Leu Met Asp
305             310             315             320

Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr Ala Glu
            325             330             335

Glu Met Leu Asp Trp Ala Asp Glu His Gly Ile Val Val Ile Asp Glu
            340             345             350

Thr Ala Ala Val Gly Phe Ser Leu Ser Leu Gly Ile Gly Phe Glu Ala
        355             360             365

Gly Asn Lys Pro Lys Glu Leu Tyr Ser Glu Glu Ala Val Asn Gly Glu
    370             375             380

Thr Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp
385             390             395             400

Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp
            405             410             415

Thr Arg Pro Gln Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Glu Ala
    420             425             430
```

```
Thr Arg Lys Leu Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val Met
        435             440             445

Phe Cys Asp Ala His Thr Asp Thr Ile Ser Asp Leu Phe Asp Val Leu
    450             455             460

Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu
465             470             475             480

Thr Ala Glu Lys Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys
            485             490             495

Leu His Gln Pro Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala
        500             505             510

Gly Leu His Ser Met Tyr Thr Asp Met Trp Ser Glu Glu Tyr Gln Cys
        515             520             525

Ala Trp Leu Asp Met Tyr His Arg Val Phe Asp Arg Val Ser Ala Val
    530             535             540

Val Gly Glu Gln Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly
545             550             555             560

Ile Leu Arg Val Gly Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp Arg
            565             570             575

Lys Pro Lys Ser Ala Ala Phe Leu Leu Gln Lys Arg Trp Thr Gly Met
            580             585             590

Asn Phe Gly Glu Lys Pro Gln Gln Gly Gly Lys Gln
        595             600
```

<210> 38

<211> 5418

<212> DNA

<213> Artificial Sequence

<220>

<223> phas-oleo GUS-phas

<220>

<221> CDS

<222> (1555)..(1908)

<223>

<220>

<221> CDS

<222> (2149)..(4125)

<223>

<400> 38

```
ctgcaggaat tcattgtact cccagtatca ttatagtgaa agttttggct ctctcgccgg        60

tggtttttta cctctatttta aaggggtttt ccacctaaaa attctggtat cattctcact       120

ttacttgtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga       180

tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc       240

ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt       300

agcgttggta gaaagcataa tgatttattc ttattcttct tcatataaat gtttaatata       360

caatataaac aaattctttta ccttaagaag gatttcccat tttatatttt aaaaatatat      420

ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa      480

aatttaactc cataatttttt ttattcgact gatcttaaag caacacccag tgacacaact      540

agccatttttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga      600

aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct      660

ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat      720

cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa      780

tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt      840

aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat      900

agtttaaagt aaatataagt aatgtagtag agtgttagag tgttaccta aaccataaac       960

tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt      1020

atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttggttc      1080

atgcatggat gcttgcgcaa gaaaaagaca agaacaaag aaaaaagaca aacagagag        1140

acaaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgtc      1200

catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatggctca      1260

cccatctcaa cccacacaca aacacattgc cttttttcttc atcatcacca caaccacctg      1320

tatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat      1380

atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata      1440

atacctataa atacctctaa tatcactcac ttctttcatc atccatccat ccagagtact      1500

actactctac tactataata ccccaacccca actcatattc aatactactc tact atg       1557
                                                                Met
```

1

```
gcg gat aca gct aga gga acc cat cac gat atc atc ggc aga gac cag        1605
Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln
            5                   10                  15

tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc gga cga        1653
Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg
            20                  25                  30

gga tct gac tac tcc aag tct agg cag att gct aaa gct gca act gct        1701
Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala
    35                  40                  45

gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt        1749
Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val
50                  55                  60                  65

gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc        1797
Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe
                70                  75                  80

agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc        1845
Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr
                85                  90                  95

ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc        1893
Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe
            100                 105                 110

tct tgg att tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa        1948
Ser Trp Ile Tyr Lys
            115

tatgtgcatg catgtgttga gccagtagct ttggatcaat tttttggtc gaataacaaa      2008

tgtaacaata agaaattgca aattctaggg aacatttggt taactaaata cgaaatttga      2068

cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggtatgat      2128

acctattgat tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac      2181
                       Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp
                           120                 125

aag ttg gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg        2229
Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu
130                 135                 140                 145

aaa gac aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat        2277
Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His
                150                 155                 160

gac cgt gac cgt act cgt ggt ggc cag cac act acc atg gtc tta cgt        2325
Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Met Val Leu Arg
            165                 170                 175

cct gta gaa acc cca acc cgt gaa atc aaa aaa ctc gac ggc ctg tgg        2373
Pro Val Glu Thr Pro Thr Arg Glu Ile Lys Lys Leu Asp Gly Leu Trp
            180                 185                 190

gca ttc agt ctg gat cgc gaa aac tgt gga att gat cag cgt tgg tgg        2421
Ala Phe Ser Leu Asp Arg Glu Asn Cys Gly Ile Asp Gln Arg Trp Trp
    195                 200                 205

gaa agc gcg tta caa gaa agc cgg gca att gct gtg cca ggc agt ttt        2469
Glu Ser Ala Leu Gln Glu Ser Arg Ala Ile Ala Val Pro Gly Ser Phe
```

```
210                    215                    220                    225

aac gat cag ttc gcc gat gca gat att cgt aat tat gcg ggc aac gtc    2517
Asn Asp Gln Phe Ala Asp Ala Asp Ile Arg Asn Tyr Ala Gly Asn Val
            230                235                240

tgg tat cag cgc gaa gtc ttt ata ccg aaa ggt tgg gca ggc cag cgt    2565
Trp Tyr Gln Arg Glu Val Phe Ile Pro Lys Gly Trp Ala Gly Gln Arg
            245                250                255

atc gtg ctg cgt ttc gat gcg gtc act cat tac ggc aaa gtg tgg gtc    2613
Ile Val Leu Arg Phe Asp Ala Val Thr His Tyr Gly Lys Val Trp Val
            260                265                270

aat aat cag gaa gtg atg gag cat cag ggc ggc tat acg cca ttt gaa    2661
Asn Asn Gln Glu Val Met Glu His Gln Gly Gly Tyr Thr Pro Phe Glu
            275                280                285

gcc gat gtc acg ccg tat gtt att gcc ggg aaa agt gta cgt atc acc    2709
Ala Asp Val Thr Pro Tyr Val Ile Ala Gly Lys Ser Val Arg Ile Thr
290                295                300                305

gtt tgt gtg aac aac gaa ctg aac tgg cag act atc ccg ccg gga atg    2757
Val Cys Val Asn Asn Glu Leu Asn Trp Gln Thr Ile Pro Pro Gly Met
            310                315                320

gtg att acc gac gaa aac ggc aag aaa aag cag tct tac ttc cat gat    2805
Val Ile Thr Asp Glu Asn Gly Lys Lys Lys Gln Ser Tyr Phe His Asp
            325                330                335

ttc ttt aac tat gcc gga atc cat cgc agc gta atg ctc tac acc acg    2853
Phe Phe Asn Tyr Ala Gly Ile His Arg Ser Val Met Leu Tyr Thr Thr
            340                345                350

ccg aac acc tgg gtg gac gat atc acc gtg gtg acg cat gtc gcg caa    2901
Pro Asn Thr Trp Val Asp Asp Ile Thr Val Val Thr His Val Ala Gln
            355                360                365

gac tgt aac cac gcg tct gtt gac tgg cag gtg gtg gcc aat ggt gat    2949
Asp Cys Asn His Ala Ser Val Asp Trp Gln Val Val Ala Asn Gly Asp
370                375                380                385

gtc agc gtt gaa ctg cgt gat gcg gat caa cag gtg gtt gca act gga    2997
Val Ser Val Glu Leu Arg Asp Ala Asp Gln Gln Val Val Ala Thr Gly
            390                395                400

caa ggc act agc ggg act ttg caa gtg gtg aat ccg cac ctc tgg caa    3045
Gln Gly Thr Ser Gly Thr Leu Gln Val Val Asn Pro His Leu Trp Gln
            405                410                415

ccg ggt gaa ggt tat ctc tat gaa ctg tgc gtc aca gcc aaa agc cag    3093
Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Cys Val Thr Ala Lys Ser Gln
            420                425                430

aca gag tgt gat atc tac ccg ctt cgc gtc ggc atc cgg tca gtg gca    3141
Thr Glu Cys Asp Ile Tyr Pro Leu Arg Val Gly Ile Arg Ser Val Ala
            435                440                445

gtg aag ggc caa cag ttc ctg att aac cac aaa ccg ttc tac ttt act    3189
Val Lys Gly Gln Gln Phe Leu Ile Asn His Lys Pro Phe Tyr Phe Thr
450                455                460                465

ggc ttt ggt cgt cat gaa gat gcg gac tta cgt ggc aaa gga ttc gat    3237
Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg Gly Lys Gly Phe Asp
            470                475                480
```

```
aac gtg ctg atg gtg cac gac cac gca tta atg gac tgg att ggg gcc       3285
Asn Val Leu Met Val His Asp His Ala Leu Met Asp Trp Ile Gly Ala
            485               490               495

aac tcc tac cgt acc tcg cat tac cct tac gct gaa gag atg ctc gac       3333
Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu Met Leu Asp
            500               505               510

tgg gca gat gaa cat ggc atc gtg gtg att gat gaa act gct gct gtc       3381
Trp Ala Asp Glu His Gly Ile Val Val Ile Asp Glu Thr Ala Ala Val
            515               520               525

ggc ttt tcg ctc tct tta ggc att ggt ttc gaa gcg ggc aac aag ccg       3429
Gly Phe Ser Leu Ser Leu Gly Ile Gly Phe Glu Ala Gly Asn Lys Pro
530               535               540               545

aaa gaa ctg tac agc gaa gag gca gtc aac ggg gaa act cag caa gcg       3477
Lys Glu Leu Tyr Ser Glu Glu Ala Val Asn Gly Glu Thr Gln Gln Ala
            550               555               560

cac tta cag gcg att aaa gag ctg ata gcg cgt gac aaa aac cac cca       3525
His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp Lys Asn His Pro
            565               570               575

agc gtg gtg atg tgg agt att gcc aac gaa ccg gat acc cgt ccg caa       3573
Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp Thr Arg Pro Gln
            580               585               590

ggt gca cgg gaa tat ttc gcg cca ctg gcg gaa gca acg cgt aaa ctc       3621
Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Glu Ala Thr Arg Lys Leu
            595               600               605

gac ccg acg cgt ccg atc acc tgc gtc aat gta atg ttc tgc gac gct       3669
Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val Met Phe Cys Asp Ala
610               615               620               625

cac acc gat acc atc agc gat ctc ttt gat gtg ctg tgc ctg aac cgt       3717
His Thr Asp Thr Ile Ser Asp Leu Phe Asp Val Leu Cys Leu Asn Arg
            630               635               640

tat tac gga tgg tat gtc caa agc ggc gat ttg gaa acg gca gag aag       3765
Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu Thr Ala Glu Lys
            645               650               655

gta ctg gaa aaa gaa ctt ctg gcc tgg cag gag aaa ctg cat cag ccg       3813
Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys Leu His Gln Pro
            660               665               670

att atc atc acc gaa tac ggc gtg gat acg tta gcc ggg ctg cac tca       3861
Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala Gly Leu His Ser
675               680               685

atg tac acc gac atg tgg agt gaa gag tat cag tgt gca tgg ctg gat       3909
Met Tyr Thr Asp Met Trp Ser Glu Glu Tyr Gln Cys Ala Trp Leu Asp
690               695               700               705

atg tat cac cgc gtc ttt gat cgc gtc agc gcc gtc gtc ggt gaa cag       3957
Met Tyr His Arg Val Phe Asp Arg Val Ser Ala Val Val Gly Glu Gln
            710               715               720

gta tgg aat ttc gcc gat ttt gcg acc tcg caa ggc ata ttg cgc gtt       4005
Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Ile Leu Arg Val
            725               730               735

ggc ggt aac aag aaa ggg atc ttc act cgc gac cgc aaa ccg aag tcg       4053
Gly Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp Arg Lys Pro Lys Ser
```

```
          740                  745                  750
gcg gct ttt ctg ctg caa aaa cgc tgg act ggc atg aac ttc ggt gaa    4101
Ala Ala Phe Leu Leu Gln Lys Arg Trp Thr Gly Met Asn Phe Gly Glu
    755                  760                  765

aaa ccg cag cag gga ggc aaa caa tgaatcaaca actctcctgg cgcaccatcg    4155
Lys Pro Gln Gln Gly Gly Lys Gln
770                  775

tcggctacag cctcggtgga attcgatatc aagcttaaat aagtatgaac taaaatgcat    4215

gtaggtgtaa gagctcatgg agagcatgga atattgtatc cgaccatgta acagtataat    4275

aactgagctc catctcactt cttctatgaa taaacaaagg atgttatgat atattaacac    4335

tctatctatg caccttattg ttctatgata aatttcctct tattattata aatcatctga    4395

atcgtgacgg cttatggaat gcttcaaata gtacaaaaac aaatgtgtac tataagactt    4455

tctaaacaat tctaacttta gcattgtgaa cgagacataa gtgttaagaa gacataacaa    4515

ttataatgga agaagtttgt ctccatttat atattatata ttacccactt atgtattata    4575

ttaggatgtt aaggagacat aacaattata aagagagaag tttgtatcca tttatatatt    4635

atatactacc catttatata ttatacttat ccacttattt aatgtcttta taaggtttga    4695

tccatgatat ttctaatatt ttagttgata tgtatatgaa agggtactat ttgaactctc    4755

ttactctgta taaaggttgg atcatcctta aagtgggtct atttaatttt attgcttctt    4815

acagataaaa aaaaaattat gagttggttt gataaaatat tgaaggattt aaaataataa    4875

taaataataa ataacatata atatatgtat ataaatttat tataatataa catttatcta    4935

taaaaaagta aatattgtca taaatctata caatcgttta gccttgctgg acgactctca    4995

attatttaaa cgagagtaaa catatttgac tttttggtta tttaacaaat tattattttaa   5055

cactatatga aatttttttt ttttatcggc aaggaaataa aattaaatta ggagggacaa    5115

tggtgtgtcc caatccttat acaaccaact tccacaggaa ggtcaggtcg gggacaacaa    5175

aaaaacaggc aagggaaatt ttttaatttg ggttgtcttg tttgctgcat aatttatgca    5235

gtaaaacact acacataacc cttttagcag tagagcaatg gttgaccgtg tgcttagctt    5295

cttttatttt atttttttat cagcaaagaa taaataaaat aaaatgagac acttcaggga    5355

tgtttcaacc cttatacaaa accccaaaaa caagtttcct agcaccctac caactaaggt    5415

acc                                                                 5418
```

<210> 39

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> phas-oleo GUS-phas

<400> 39

Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
1   5   10   15

Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
            20   25   30

Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
        35   40   45

Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
    50   55   60

Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65   70   75   80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
            85   90   95

Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
            100   105   110

Phe Ser Trp Ile Tyr Lys
        115

<210> 40

<211> 659

<212> PRT

<213> Artificial Sequence

<220>

<223> phas-oleo GUS-phas

<400> 40

Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1   5   10   15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
            20   25   30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
        35   40   45

Arg Gly Gly Gln His Thr Thr Met Val Leu Arg Pro Val Glu Thr Pro

- 117 -

```
          50                    55                    60

Thr Arg Glu Ile Lys Lys Leu Asp Gly Leu Trp Ala Phe Ser Leu Asp
65                  70                  75                  80

Arg Glu Asn Cys Gly Ile Asp Gln Arg Trp Trp Glu Ser Ala Leu Gln
                85                  90                  95

Glu Ser Arg Ala Ile Ala Val Pro Gly Ser Phe Asn Asp Gln Phe Ala
            100                 105                 110

Asp Ala Asp Ile Arg Asn Tyr Ala Gly Asn Val Trp Tyr Gln Arg Glu
            115                 120                 125

Val Phe Ile Pro Lys Gly Trp Ala Gly Gln Arg Ile Val Leu Arg Phe
        130                 135                 140

Asp Ala Val Thr His Tyr Gly Lys Val Trp Val Asn Asn Gln Glu Val
145                 150                 155                 160

Met Glu His Gln Gly Gly Tyr Thr Pro Phe Glu Ala Asp Val Thr Pro
                165                 170                 175

Tyr Val Ile Ala Gly Lys Ser Val Arg Ile Thr Val Cys Val Asn Asn
            180                 185                 190

Glu Leu Asn Trp Gln Thr Ile Pro Pro Gly Met Val Ile Thr Asp Glu
        195                 200                 205

Asn Gly Lys Lys Lys Gln Ser Tyr Phe His Asp Phe Phe Asn Tyr Ala
    210                 215                 220

Gly Ile His Arg Ser Val Met Leu Tyr Thr Thr Pro Asn Thr Trp Val
225                 230                 235                 240

Asp Asp Ile Thr Val Val Thr His Val Ala Gln Asp Cys Asn His Ala
            245                 250                 255

Ser Val Asp Trp Gln Val Val Ala Asn Gly Asp Val Ser Val Glu Leu
            260                 265                 270

Arg Asp Ala Asp Gln Gln Val Val Ala Thr Gly Gln Gly Thr Ser Gly
        275                 280                 285

Thr Leu Gln Val Val Asn Pro His Leu Trp Gln Pro Gly Glu Gly Tyr
    290                 295                 300

Leu Tyr Glu Leu Cys Val Thr Ala Lys Ser Gln Thr Glu Cys Asp Ile
305                 310                 315                 320
```

Tyr Pro Leu Arg Val Gly Ile Arg Ser Val Ala Val Lys Gly Gln Gln
                325   330   335

Phe Leu Ile Asn His Lys Pro Phe Tyr Phe Thr Gly Phe Gly Arg His
            340   345   350

Glu Asp Ala Asp Leu Arg Gly Lys Gly Phe Asp Asn Val Leu Met Val
            355   360   365

His Asp His Ala Leu Met Asp Trp Ile Gly Ala Asn Ser Tyr Arg Thr
    370   375   380

Ser His Tyr Pro Tyr Ala Glu Glu Met Leu Asp Trp Ala Asp Glu His
385   390   395   400

Gly Ile Val Val Ile Asp Glu Thr Ala Ala Val Gly Phe Ser Leu Ser
            405   410   415

Leu Gly Ile Gly Phe Glu Ala Gly Asn Lys Pro Lys Glu Leu Tyr Ser
            420   425   430

Glu Glu Ala Val Asn Gly Glu Thr Gln Gln Ala His Leu Gln Ala Ile
        435   440   445

Lys Glu Leu Ile Ala Arg Asp Lys Asn His Pro Ser Val Val Met Trp
    450   455   460

Ser Ile Ala Asn Glu Pro Asp Thr Arg Pro Gln Gly Ala Arg Glu Tyr
465   470   475   480

Phe Ala Pro Leu Ala Glu Ala Thr Arg Lys Leu Asp Pro Thr Arg Pro
            485   490   495

Ile Thr Cys Val Asn Val Met Phe Cys Asp Ala His Thr Asp Thr Ile
            500   505   510

Ser Asp Leu Phe Asp Val Leu Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr
        515   520   525

Val Gln Ser Gly Asp Leu Glu Thr Ala Glu Lys Val Leu Glu Lys Glu
    530   535   540

Leu Leu Ala Trp Gln Glu Lys Leu His Gln Pro Ile Ile Ile Thr Glu
545   550   555   560

Tyr Gly Val Asp Thr Leu Ala Gly Leu His Ser Met Tyr Thr Asp Met
            565   570   575

Trp Ser Glu Glu Tyr Gln Cys Ala Trp Leu Asp Met Tyr His Arg Val

```
          580                    585                    590
```

Phe Asp Arg Val Ser Ala Val Val Gly Glu Gln Val Trp Asn Phe Ala
    595   600   605

Asp Phe Ala Thr Ser Gln Gly Ile Leu Arg Val Gly Gly Asn Lys Lys
    610   615   620

Gly Ile Phe Thr Arg Asp Arg Lys Pro Lys Ser Ala Ala Phe Leu Leu
625   630   635   640

Gln Lys Arg Trp Thr Gly Met Asn Phe Gly Glu Lys Pro Gln Gln Gly
            645   650   655

Gly Lys Gln

<210>   41

<211>   5390

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   phas-caleo-GUS-phas

<220>

<221>   CDS

<222>   (1548)..(4097)

<223>


```
<400> 41
gaattcattg tactcccagt atcattatag tgaaagtttt ggctctctcg ccggtggttt     60

tttacctcta tttaaagggg ttttccacct aaaaattctg gtatcattct cactttactt    120

gttactttaa tttctcataa tctttggttg aaattatcac gcttccgcac acgatatccc    180

tacaaattta ttatttgtta aacattttca aaccgcataa aattttatga agtcccgtct    240

atctttaatg tagtctaaca ttttcatatt gaaatatata atttacttaa ttttagcgtt    300

ggtagaaagc ataaagattt attcttattc ttcttcatat aaatgtttaa tatacaatat    360

aaacaaattc tttaccttaa gaaggatttc ccattttata tttaaaaat atatttatca    420

aatattttc aaccacgtaa atctcataat aataagttgt ttcaaaagta ataaaattta    480

actccataat tttttattc gactgatctt aaagcaacac ccagtgacac aactagccat    540
```

```
tttttttcttt gaataaaaaa atccaattat cattgtattt tttttataca atgaaaattt   600

caccaaacaa tcatttgtgg tatttctgaa gcaagtcatg ttatgcaaaa ttctataatt   660

cccatttgac actacggaag taactgaaga tctgctttta catgcgagac acatcttcta   720

aagtaatttt aataatagtt actatattca agatttcata tatcaaatac tcaatattac   780

ttctaaaaaa ttaattagat ataattaaaa tattactttt ttaattttaa gtttaattgt   840

tgaatttgtg actattgatt tattattcta ctatgtttaa attgttttat agatagttta   900

aagtaaatat aagtaatgta gtagagtgtt agagtgttac cctaaaccat aaactataac   960

atttatggtg gactaatttt catatatttc ttattgcttt tacctttttct tggtatgtaa  1020

gtccgtaact agaattacag tgggttgcca tgacactctg tggtcttttg gttcatgcat  1080

gggtcttgcg caagaaaaag acaaagaaca aagaaaaaag acaaaacaga gagacaaaac  1140

gcaatcacac aaccaactca aattagtcac tggctgatca agatcgccgc gtccatgtat  1200

gtctaaatgc catgcaaagc aacacgtgct taacatgcac tttaaatggc tcacccatct  1260

caacccacac acaaacacat tgccttttttc ttcatcatca ccacaaccac ctgtatatat  1320

tcattctctt ccgccacctc aatttcttca cttcaacaca cgtcaacctg catatgcgtg  1380

tcatcccatg cccaaatctc catgcatgtt ccaaccacct tctctcttat ataataccta  1440

taaatacctc taatatcact cacttctttc atcatccatc catccagagt actactactc  1500

tactactata ataccccaac ccaactcata ttcaatacta ctctacc atg ggg tca    1556
                                                     Met Gly Ser
                                                      1

aag acg gag atg atg gag aga gac gca atg gct acg gtg gct ccc tat   1604
Lys Thr Glu Met Met Glu Arg Asp Ala Met Ala Thr Val Ala Pro Tyr
  5               10                  15

gcg ccg gtc act tac cac cgc cgt gct cgt gtt gac ttg gat gat aga   1652
Ala Pro Val Thr Tyr His Arg Arg Ala Arg Val Asp Leu Asp Asp Arg
 20               25                  30                  35

ctt cct aaa cct tat atg cca aga gca ttg caa gca cca gac aga gaa   1700
Leu Pro Lys Pro Tyr Met Pro Arg Ala Leu Gln Ala Pro Asp Arg Glu
              40                  45                  50

cac ccg tac gga act cca ggc cat aag aat tac gga ctt agt gtt ctt   1748
His Pro Tyr Gly Thr Pro Gly His Lys Asn Tyr Gly Leu Ser Val Leu
              55                  60                  65

caa cag cat gtc tcc ttc ttc gat atc gat gat aat ggc atc att tac   1796
Gln Gln His Val Ser Phe Phe Asp Ile Asp Asp Asn Gly Ile Ile Tyr
          70                  75                  80

cct tgg gag acc tac tct gga ctg cga atg ctt ggt ttc aat atc att   1844
Pro Trp Glu Thr Tyr Ser Gly Leu Arg Met Leu Gly Phe Asn Ile Ile
          85                  90                  95

ggg tcg ctt ata ata gcc gct gtt atc aac ctg acc ctt agc tat gcc   1892
Gly Ser Leu Ile Ile Ala Ala Val Ile Asn Leu Thr Leu Ser Tyr Ala
100                 105                 110                 115

act ctt ccg ggg tgg tta cct tca cct ttc ttc cct ata tac ata cac   1940
Thr Leu Pro Gly Trp Leu Pro Ser Pro Phe Phe Pro Ile Tyr Ile His
```

```
                  120                    125                    130

aac ata cac aag tca aag cat gga agt gat tca aaa aca tat gac aat    1988
Asn Ile His Lys Ser Lys His Gly Ser Asp Ser Lys Thr Tyr Asp Asn
            135                    140                    145

gaa gga agg ttt atg ccg gtg aat ctt gag ttg ata ttt agc aaa tat    2036
Glu Gly Arg Phe Met Pro Val Asn Leu Glu Leu Ile Phe Ser Lys Tyr
            150                    155                    160

gcg aaa acc ttg cca gac aag ttg agt ctt gga gaa cta tgg gag atg    2084
Ala Lys Thr Leu Pro Asp Lys Leu Ser Leu Gly Glu Leu Trp Glu Met
            165                    170                    175

aca gaa gga aac cgt gac gct tgg gac att ttt gga tgg atc gca ggc    2132
Thr Glu Gly Asn Arg Asp Ala Trp Asp Ile Phe Gly Trp Ile Ala Gly
180                    185                    190                    195

aaa ata gag tgg gga ctg ttg tac ttg cta gca agg gat gaa gaa ggg    2180
Lys Ile Glu Trp Gly Leu Leu Tyr Leu Leu Ala Arg Asp Glu Glu Gly
                  200                    205                    210

ttt ttg tca aaa gaa gct att agg cgg tgt ttc gat gga agc ttg ttc    2228
Phe Leu Ser Lys Glu Ala Ile Arg Arg Cys Phe Asp Gly Ser Leu Phe
            215                    220                    225

gag tac tgt gcc aaa atc tac gct ggt atc agt gaa gac aag aca gca    2276
Glu Tyr Cys Ala Lys Ile Tyr Ala Gly Ile Ser Glu Asp Lys Thr Ala
            230                    235                    240

tac tac gcc atg gtc tta cgt cct gta gaa acc cca acc cgt gaa atc    2324
Tyr Tyr Ala Met Val Leu Arg Pro Val Glu Thr Pro Thr Arg Glu Ile
            245                    250                    255

aaa aaa ctc gac ggc ctg tgg gca ttc agt ctg gat cgc gaa aac tgt    2372
Lys Lys Leu Asp Gly Leu Trp Ala Phe Ser Leu Asp Arg Glu Asn Cys
260                    265                    270                    275

gga att gat cag cgt tgg tgg gaa agc gcg tta caa gaa agc cgg gca    2420
Gly Ile Asp Gln Arg Trp Trp Glu Ser Ala Leu Gln Glu Ser Arg Ala
                  280                    285                    290

att gct gtg cca ggc agt ttt aac gat cag ttc gcc gat gca gat att    2468
Ile Ala Val Pro Gly Ser Phe Asn Asp Gln Phe Ala Asp Ala Asp Ile
                  295                    300                    305

cgt aat tat gcg ggc aac gtc tgg tat cag cgc gaa gtc ttt ata ccg    2516
Arg Asn Tyr Ala Gly Asn Val Trp Tyr Gln Arg Glu Val Phe Ile Pro
            310                    315                    320

aaa ggt tgg gca ggc cag cgt atc gtg ctg cgt ttc gat gcg gtc act    2564
Lys Gly Trp Ala Gly Gln Arg Ile Val Leu Arg Phe Asp Ala Val Thr
            325                    330                    335

cat tac ggc aaa gtg tgg gtc aat aat cag gaa gtg atg gag cat cag    2612
His Tyr Gly Lys Val Trp Val Asn Asn Gln Glu Val Met Glu His Gln
340                    345                    350                    355

ggc ggc tat acg cca ttt gaa gcc gat gtc acg ccg tat gtt att gcc    2660
Gly Gly Tyr Thr Pro Phe Glu Ala Asp Val Thr Pro Tyr Val Ile Ala
                  360                    365                    370

ggg aaa agt gta cgt atc acc gtt tgt gtg aac aac gaa ctg aac tgg    2708
Gly Lys Ser Val Arg Ile Thr Val Cys Val Asn Asn Glu Leu Asn Trp
            375                    380                    385
```

```
cag act atc ccg ccg gga atg gtg att acc gac gaa aac ggc aag aaa      2756
Gln Thr Ile Pro Pro Gly Met Val Ile Thr Asp Glu Asn Gly Lys Lys
        390             395             400

aag cag tct tac ttc cat gat ttc ttt aac tat gcc gga atc cat cgc      2804
Lys Gln Ser Tyr Phe His Asp Phe Phe Asn Tyr Ala Gly Ile His Arg
        405             410             415

agc gta atg ctc tac acc acg ccg aac acc tgg gtg gac gat atc acc      2852
Ser Val Met Leu Tyr Thr Thr Pro Asn Thr Trp Val Asp Asp Ile Thr
420             425             430             435

gtg gtg acg cat gtc gcg caa gac tgt aac cac gcg tct gtt gac tgg      2900
Val Val Thr His Val Ala Gln Asp Cys Asn His Ala Ser Val Asp Trp
                440             445             450

cag gtg gtg gcc aat ggt gat gtc agc gtt gaa ctg cgt gat gcg gat      2948
Gln Val Val Ala Asn Gly Asp Val Ser Val Glu Leu Arg Asp Ala Asp
                455             460             465

caa cag gtg gtt gca act gga caa ggc act agc ggg act ttg caa gtg      2996
Gln Gln Val Val Ala Thr Gly Gln Gly Thr Ser Gly Thr Leu Gln Val
                470             475             480

gtg aat ccg cac ctc tgg caa ccg ggt gaa ggt tat ctc tat gaa ctg      3044
Val Asn Pro His Leu Trp Gln Pro Gly Glu Gly Tyr Leu Tyr Glu Leu
        485             490             495

tgc gtc aca gcc aaa agc cag aca gag tgt gat atc tac ccg ctt cgc      3092
Cys Val Thr Ala Lys Ser Gln Thr Glu Cys Asp Ile Tyr Pro Leu Arg
500             505             510             515

gtc ggc atc cgg tca gtg gca gtg aag ggc caa cag ttc ctg att aac      3140
Val Gly Ile Arg Ser Val Ala Val Lys Gly Gln Gln Phe Leu Ile Asn
                520             525             530

cac aaa ccg ttc tac ttt act ggc ttt ggt cgt cat gaa gat gcg gac      3188
His Lys Pro Phe Tyr Phe Thr Gly Phe Gly Arg His Glu Asp Ala Asp
                535             540             545

tta cgt ggc aaa gga ttc gat aac gtg ctg atg gtg cac gac cac gca      3236
Leu Arg Gly Lys Gly Phe Asp Asn Val Leu Met Val His Asp His Ala
                550             555             560

tta atg gac tgg att ggg gcc aac tcc tac cgt acc tcg cat tac cct      3284
Leu Met Asp Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro
        565             570             575

tac gct gaa gag atg ctc gac tgg gca gat gaa cat ggc atc gtg gtg      3332
Tyr Ala Glu Glu Met Leu Asp Trp Ala Asp Glu His Gly Ile Val Val
580             585             590             595

att gat gaa act gct gct gtc ggc ttt tcg ctc tct tta ggc att ggt      3380
Ile Asp Glu Thr Ala Ala Val Gly Phe Ser Leu Ser Leu Gly Ile Gly
                600             605             610

ttc gaa gcg ggc aac aag ccg aaa gaa ctg tac agc gaa gag gca gtc      3428
Phe Glu Ala Gly Asn Lys Pro Lys Glu Leu Tyr Ser Glu Glu Ala Val
                615             620             625

aac ggg gaa act cag caa gcg cac tta cag gcg att aaa gag ctg ata      3476
Asn Gly Glu Thr Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu Ile
                630             635             640

gcg cgt gac aaa aac cac cca agc gtg gtg atg tgg agt att gcc aac      3524
Ala Arg Asp Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn
```

```
        645                    650                   655

gaa ccg gat acc cgt ccg caa ggt gca cgg gaa tat ttc gcg cca ctg   3572
Glu Pro Asp Thr Arg Pro Gln Gly Ala Arg Glu Tyr Phe Ala Pro Leu
660                 665                 670                 675

gcg gaa gca acg cgt aaa ctc gac ccg acg cgt ccg atc acc tgc gtc   3620
Ala Glu Ala Thr Arg Lys Leu Asp Pro Thr Arg Pro Ile Thr Cys Val
                680                 685                 690

aat gta atg ttc tgc gac gct cac acc gat acc atc agc gat ctc ttt   3668
Asn Val Met Phe Cys Asp Ala His Thr Asp Thr Ile Ser Asp Leu Phe
                695                 700                 705

gat gtg ctg tgc ctg aac cgt tat tac gga tgg tat gtc caa agc ggc   3716
Asp Val Leu Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly
            710                 715                 720

gat ttg gaa acg gca gag aag gta ctg gaa aaa gaa ctt ctg gcc tgg   3764
Asp Leu Glu Thr Ala Glu Lys Val Leu Glu Lys Glu Leu Leu Ala Trp
        725                 730                 735

cag gag aaa ctg cat cag ccg att atc atc acc gaa tac ggc gtg gat   3812
Gln Glu Lys Leu His Gln Pro Ile Ile Ile Thr Glu Tyr Gly Val Asp
740                 745                 750                 755

acg tta gcc ggg ctg cac tca atg tac acc gac atg tgg agt gaa gag   3860
Thr Leu Ala Gly Leu His Ser Met Tyr Thr Asp Met Trp Ser Glu Glu
                760                 765                 770

tat cag tgt gca tgg ctg gat atg tat cac cgc gtc ttt gat cgc gtc   3908
Tyr Gln Cys Ala Trp Leu Asp Met Tyr His Arg Val Phe Asp Arg Val
                775                 780                 785

agc gcc gtc gtc ggt gaa cag gta tgg aat ttc gcc gat ttt gcg acc   3956
Ser Ala Val Val Gly Glu Gln Val Trp Asn Phe Ala Asp Phe Ala Thr
                790                 795                 800

tcg caa ggc ata ttg cgc gtt ggc ggt aac aag aaa ggg atc ttc act   4004
Ser Gln Gly Ile Leu Arg Val Gly Gly Asn Lys Lys Gly Ile Phe Thr
        805                 810                 815

cgc gac cgc aaa ccg aag tcg gcg gct ttt ctg ctg caa aaa cgc tgg   4052
Arg Asp Arg Lys Pro Lys Ser Ala Ala Phe Leu Leu Gln Lys Arg Trp
820                 825                 830                 835

act ggc atg aac ttc ggt gaa aaa ccg cag cag gga ggc aaa caa       4097
Thr Gly Met Asn Phe Gly Glu Lys Pro Gln Gln Gly Gly Lys Gln
                840                 845                 850

tgaatcaaca actctcctgg cgcaccatcg tcggctacag cctcggtgga attcgatatc   4157

aagcttaaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg agagcatgga   4217

atattgtatc cgaccatgta acagtataat aactgagctc catctcactt cttctatgaa   4277

taaacaaagg atgttatgat atattaacac tctatctatg caccttattg ttctatgata   4337

aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat gcttcaaata   4397

gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta gcattgtgaa   4457

cgagacataa gtgttaagaa gacataacaa ttataatgga agaagtttgt ctccatttat   4517

atattatata ttacccactt atgtattata ttaggatgtt aaggagacat aacaattata   4577
```

```
aagagagaag tttgtatcca tttatatatt atatactacc catttatata ttatacttat   4637

ccacttattt aatgtcttta taaggtttga tccatgatat ttctaatatt ttagttgata   4697

tgtatatgaa agggtactat ttgaactctc ttactctgta taaaggttgg atcatcctta   4757

aagtgggtct atttaatttt attgcttctt acagataaaa aaaaaattat gagttggttt   4817

gataaaatat tgaaggattt aaaataataa taaataataa ataacatata atatatgtat   4877

ataaatttat tataatataa catttatcta taaaaaagta aatattgtca taaatctata   4937

caatcgttta gccttgctgg acgactctca attatttaaa cgagagtaaa catatttgac   4997

tttttggtta tttaacaaat tattatttaa cactatatga aatttttttt ttttatcggc   5057

aaggaaataa aattaaatta ggagggacaa tggtgtgtcc caatccttat acaaccaact   5117

tccacaggaa ggtcaggtcg gggacaacaa aaaaacaggc aagggaaatt ttttaatttg   5177

ggttgtcttg tttgctgcat aatttatgca gtaaaacact acacataacc cttttagcag   5237

tagagcaatg gttgaccgtg tgcttagctt cttttatttt attttttttat cagcaaagaa   5297

taaataaaat aaaatgagac acttcaggga tgtttcaacc cttatacaaa accccaaaaa   5357

caagtttcct agcaccctac caactaaggt acc                                5390
```

<210>   42

<211>   850

<212>   PRT

<213>   Artificial Sequence

<220>

<223>   phas-caleo-GUS-phas

<400>   42

```
Met Gly Ser Lys Thr Glu Met Met Glu Arg Asp Ala Met Ala Thr Val
1               5                   10                  15


Ala Pro Tyr Ala Pro Val Thr Tyr His Arg Arg Ala Arg Val Asp Leu
            20                  25                  30


Asp Asp Arg Leu Pro Lys Pro Tyr Met Pro Arg Ala Leu Gln Ala Pro
        35                  40                  45


Asp Arg Glu His Pro Tyr Gly Thr Pro Gly His Lys Asn Tyr Gly Leu
    50                  55                  60


Ser Val Leu Gln Gln His Val Ser Phe Phe Asp Ile Asp Asp Asn Gly
65                  70                  75                  80


Ile Ile Tyr Pro Trp Glu Thr Tyr Ser Gly Leu Arg Met Leu Gly Phe
```

```
                    85                      90                          95


Asn Ile Ile Gly Ser Leu Ile Ile Ala Ala Val Ile Asn Leu Thr Leu
            100                 105                 110

Ser Tyr Ala Thr Leu Pro Gly Trp Leu Pro Ser Pro Phe Phe Pro Ile
            115                 120                 125

Tyr Ile His Asn Ile His Lys Ser Lys His Gly Ser Asp Ser Lys Thr
    130                 135                 140

Tyr Asp Asn Glu Gly Arg Phe Met Pro Val Asn Leu Glu Leu Ile Phe
145                 150                 155                 160

Ser Lys Tyr Ala Lys Thr Leu Pro Asp Lys Leu Ser Leu Gly Glu Leu
            165                 170                 175

Trp Glu Met Thr Glu Gly Asn Arg Asp Ala Trp Asp Ile Phe Gly Trp
            180                 185                 190

Ile Ala Gly Lys Ile Glu Trp Gly Leu Leu Tyr Leu Leu Ala Arg Asp
            195                 200                 205

Glu Glu Gly Phe Leu Ser Lys Glu Ala Ile Arg Arg Cys Phe Asp Gly
    210                 215                 220

Ser Leu Phe Glu Tyr Cys Ala Lys Ile Tyr Ala Gly Ile Ser Glu Asp
225                 230                 235                 240

Lys Thr Ala Tyr Tyr Ala Met Val Leu Arg Pro Val Glu Thr Pro Thr
            245                 250                 255

Arg Glu Ile Lys Lys Leu Asp Gly Leu Trp Ala Phe Ser Leu Asp Arg
            260                 265                 270

Glu Asn Cys Gly Ile Asp Gln Arg Trp Trp Glu Ser Ala Leu Gln Glu
            275                 280                 285

Ser Arg Ala Ile Ala Val Pro Gly Ser Phe Asn Asp Gln Phe Ala Asp
    290                 295                 300

Ala Asp Ile Arg Asn Tyr Ala Gly Asn Val Trp Tyr Gln Arg Glu Val
305                 310                 315                 320

Phe Ile Pro Lys Gly Trp Ala Gly Gln Arg Ile Val Leu Arg Phe Asp
            325                 330                 335

Ala Val Thr His Tyr Gly Lys Val Trp Val Asn Asn Gln Glu Val Met
            340                 345                 350
```

- 126 -

```
Glu His Gln Gly Gly Tyr Thr Pro Phe Glu Ala Asp Val Thr Pro Tyr
        355             360             365

Val Ile Ala Gly Lys Ser Val Arg Ile Thr Val Cys Val Asn Asn Glu
    370             375             380

Leu Asn Trp Gln Thr Ile Pro Pro Gly Met Val Ile Thr Asp Glu Asn
385             390             395             400

Gly Lys Lys Lys Gln Ser Tyr Phe His Asp Phe Phe Asn Tyr Ala Gly
            405             410             415

Ile His Arg Ser Val Met Leu Tyr Thr Thr Pro Asn Thr Trp Val Asp
            420             425             430

Asp Ile Thr Val Val Thr His Val Ala Gln Asp Cys Asn His Ala Ser
        435             440             445

Val Asp Trp Gln Val Val Ala Asn Gly Asp Val Ser Val Glu Leu Arg
    450             455             460

Asp Ala Asp Gln Gln Val Val Ala Thr Gly Gln Gly Thr Ser Gly Thr
465             470             475             480

Leu Gln Val Val Asn Pro His Leu Trp Gln Pro Gly Glu Gly Tyr Leu
            485             490             495

Tyr Glu Leu Cys Val Thr Ala Lys Ser Gln Thr Glu Cys Asp Ile Tyr
            500             505             510

Pro Leu Arg Val Gly Ile Arg Ser Val Ala Val Lys Gly Gln Gln Phe
        515             520             525

Leu Ile Asn His Lys Pro Phe Tyr Phe Thr Gly Phe Gly Arg His Glu
    530             535             540

Asp Ala Asp Leu Arg Gly Lys Gly Phe Asp Asn Val Leu Met Val His
545             550             555             560

Asp His Ala Leu Met Asp Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser
            565             570             575

His Tyr Pro Tyr Ala Glu Glu Met Leu Asp Trp Ala Asp Glu His Gly
        580             585             590

Ile Val Val Ile Asp Glu Thr Ala Ala Val Gly Phe Ser Leu Ser Leu
    595             600             605

Gly Ile Gly Phe Glu Ala Gly Asn Lys Pro Lys Glu Leu Tyr Ser Glu
```

```
            610                    615                    620


Glu Ala Val Asn Gly Glu Thr Gln Gln Ala His Leu Gln Ala Ile Lys
625                 630             635                 640


Glu Leu Ile Ala Arg Asp Lys Asn His Pro Ser Val Val Met Trp Ser
                645             650                 655


Ile Ala Asn Glu Pro Asp Thr Arg Pro Gln Gly Ala Arg Glu Tyr Phe
            660             665                 670


Ala Pro Leu Ala Glu Ala Thr Arg Lys Leu Asp Pro Thr Arg Pro Ile
        675             680             685


Thr Cys Val Asn Val Met Phe Cys Asp Ala His Thr Asp Thr Ile Ser
        690             695             700


Asp Leu Phe Asp Val Leu Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val
705             710             715                 720


Gln Ser Gly Asp Leu Glu Thr Ala Glu Lys Val Leu Glu Lys Glu Leu
            725             730                 735


Leu Ala Trp Gln Glu Lys Leu His Gln Pro Ile Ile Ile Thr Glu Tyr
            740             745             750


Gly Val Asp Thr Leu Ala Gly Leu His Ser Met Tyr Thr Asp Met Trp
        755             760             765


Ser Glu Glu Tyr Gln Cys Ala Trp Leu Asp Met Tyr His Arg Val Phe
    770             775             780


Asp Arg Val Ser Ala Val Val Gly Glu Gln Val Trp Asn Phe Ala Asp
785             790             795                 800


Phe Ala Thr Ser Gln Gly Ile Leu Arg Val Gly Gly Asn Lys Lys Gly
            805             810                 815


Ile Phe Thr Arg Asp Arg Lys Pro Lys Ser Ala Ala Phe Leu Leu Gln
            820             825             830


Lys Arg Trp Thr Gly Met Asn Phe Gly Glu Lys Pro Gln Gln Gly Gly
        835             840             845


Lys Gln
850
```